What is claimed is:

1. A method for designing a specific polyamide

$$X_1X_2 \ldots X_m\text{-}\gamma\text{-}X_{(m+1)} \ldots X_{(2m-1)}X_{2m}$$

wherein X_1, X_2, X_m, $X_{(m+1)}$, $X_{(2m-1)}$, and X_{2m} are carboxamide residues forming carboxamide binding pairs X_1/X_{2m}, $X_2/X_{(2m-1)}$, $X_m/X_{(m+1)}$, and γ is γ-aminobuytic acid or 2,4 diaminobutyric acid and Dp is dimethylaminopropylamide, suitable for use as a DNA-binding ligand that is selective for identified target DNA sequences 5'-$WN_1N_2 \ldots N_mW$-3' where m is an integer having a value from 3 to 6, comprising the steps of:

a. identifying a target sequence of double stranded DNA having the form 5'-$WN_1N_2 \ldots N_mW$-3', $N_1N_2 \ldots N_m$ being the sequence to be bound by carboxamide residues, wherein each N is independently chosen from the group A, G, C, and T, each W is independently chosen from the group A and T, and m is an integer having a value from 3 to 6;

b. representing the identified sequence as 5'-W***ab*** **. . .** ***x***W-3', wherein ***a*** is a first nucleotide to be bound by the X_1 carboxamide residue, ***b*** is a second nucleotide to be bound by the X_2 carboxamide residue, and ***x*** is the corresponding nucleotide to be bound by the X_m carboxamide residue;

c. defining ***a*** as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified sequence;

d. selecting Im as the X_1 carboxamide residue and Py as the X_{2m} carboxamide residue if ***a*** = G;

e. selecting Py as the X_1 carboxamide residue and Im as the X_{2m} carboxamide residue if ***a*** = C;

f. selecting Hp as the X_1 carboxamide residue and Py as the X_{2m} carboxamide residue if ***a*** = T;

g. selecting Py as the X_1 carboxamide residue and Hp as the X_{2m} carboxamide residue if ***a*** = A; and

h. repeating steps c – g for ***b*** through ***x*** until all carboxamide residues are selected.

2. The method of claim 1 further comprising the step of synthesizing the polyamide

$$X_1X_2 \ldots X_m\text{-}\gamma\text{-}X_{(m+1)} \ldots X_{(2m-1)}X_{2m}.$$

3. The method of claim 2 further comprising the step of determining if the binding affinity of the polyamide to the identified sequence is subnanomolar.

SUB 2 D cont'd

4. The method of claim 2 further comprising the step of determining if the sequence specificity of the polyamide is greater or equal to ten.

5. The method of claim 2 further comprising the step of replacing at least one pyrrole residue with a β-alanine residue.

6. A method for designing a selective polyamide molecule $X_1X_2X_3X_4$-γ-$X_5X_6X_7X_8$, wherein X_1, X_2, X_3, X_4, X_5, X_6, X_7, and X_8, are carboxamide residues forming binding pairs X_1/X_8, X_2/X_7, X_3/X_6 and X_4/X_5, and γ is γ-aminobuytic acid or 2,4 diaminobutyric acid suitable for binding to a six base pair sequence of the form 5'-WNNNNW-3' in the minor groove of double stranded DNA, comprising the steps of:

a. identifying a six base pair sequence of double stranded DNA having the form 5'-WNNNNW-3', wherein W is either A or T, NNNN is the sequence to be bound by carboxamide residues, and each N is independently A, G, C, or T;

b. representing the identified sequence as 5'-W***abcd***W-3', wherein ***a*** is a first nucleotide to be bound by a carboxamide residue, ***b*** is a second nucleotide to be bound by a carboxamide residue, ***c*** is a third nucleotide to be bound by a carboxamide residue, and ***d*** is a fourth nucleotide to be bound by a carboxamide residue;

c. defining ***a*** as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

d. selecting Im as the X_1 carboxamide residue and Py as the X_8 carboxamide residue if ***a*** = G;

e. selecting Py as the X_1 carboxamide residue and Im as the X_8 carboxamide residue if ***a*** = C;

f. selecting Hp as the X_1 carboxamide residue and Py as the X_8 carboxamide residue if ***a*** = T;

g. selecting Py as the X_1 carboxamide residue and Hp as the X_8 carboxamide residue if ***a*** = A;

h. defining ***b*** as A, G, C, or T to correspond to the second nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

i. selecting Im as the X_2 carboxamide residue and Py as the X_7 carboxamide residue if ***b*** = G;

j. selecting Py as the X_2 carboxamide residue and Im as the X_7 carboxamide residue if ***b*** = C;

k. selecting Hp as the X_2 carboxamide residue and Py as the X_7 carboxamide residue if ***b*** = T;

l. selecting Py as the X_2 carboxamide residue and Hp as the X_7 carboxamide residue if ***b*** = A;

m. defining ***c*** as A, G, C, or T to correspond to the third nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

n. selecting Im as the X_3 carboxamide residue and Py as the X_6 carboxamide residue if ***c*** = G;

o. selecting Py as the X_3 carboxamide residue and Im as the X_6 carboxamide residue if ***c*** = C;

p. selecting Hp as the X_3 carboxamide residue and Py as the X_6 carboxamide residue if ***c*** = T;

q. selecting Py as the X_3 carboxamide residue and Hp as the X_6 carboxamide residue if ***c*** = A;

r. defining ***d*** as A, G, C, or T to correspond to the fourth nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

s. selecting Im as the X_4 carboxamide residue and Py as the X_5 carboxamide residue if ***d*** = G;

t. selecting Py as the X_4 carboxamide residue and Im as the X_5 carboxamide residue if ***d*** = C;

u. selecting Hp as the X_4 carboxamide residue and Py as the X_5 carboxamide residue if ***d*** = T; and

v. selecting Py as the X_4 carboxamide residue and Hp as the X_5 carboxamide residue if ***d*** = A.

7. The method of claim 6 further comprising the step of synthesizing the polyamide $X_1X_2X_3X_4$-γ-$X_5X_6X_7X_8$.

8. The method of claim 7 further comprising the step of determining if the binding affinity of the polyamide to the identified sequence is subnanomolar.

9. The method of claim 7 further comprising the step of determining if the sequence specificity of the polyamide is greater or equal to ten.

10. The method of claim 7 further comprising the step of replacing at least one pyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_6, and X_7.

11. The method of claim 7 further comprising the step of replacing at least one 3-hydroxypyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_6, and X_7.

12. A polyamide composition produced by the process comprising the steps of:

a. identifying a six base pair sequence of double stranded DNA having the form 5'-WNNNNW-3', wherein W is either A or T, NNNN is the sequence to be bound by carboxamide residues, and each N is independently A, G, C, or T;

b. representing the identified sequence as 5'-W***abcd***W-3', wherein ***a*** is a first nucleotide to be bound by a carboxamide residue, ***b*** is a second nucleotide to be bound by a carboxamide residue, ***c*** is a third nucleotide to be bound by a carboxamide residue, and ***d*** is a fourth nucleotide to be bound by a carboxamide residue;

c. defining ***a*** as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

d. selecting Im as the X_1 carboxamide residue and Py as the X_8 carboxamide residue if ***a*** = G;

e. selecting Py as the X_1 carboxamide residue and Im as the X_8 carboxamide residue if ***a*** = C;

f. selecting Hp as the X_1 carboxamide residue and Py as the X_8 carboxamide residue if ***a*** = T;

g. selecting Py as the X_1 carboxamide residue and Hp as the X_8 carboxamide residue if ***a*** = A;

h. defining ***b*** as A, G, C, or T to correspond to the second nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

i. selecting Im as the X_2 carboxamide residue and Py as the X_7 carboxamide residue if ***b*** = G;

j. selecting Py as the X_2 carboxamide residue and Im as the X_7 carboxamide residue if ***b*** = C;

k. selecting Hp as the X_2 carboxamide residue and Py as the X_7 carboxamide residue if ***b*** = T;

l. selecting Py as the X_2 carboxamide residue and Hp as the X_7 carboxamide residue if ***b*** = A;

m. defining ***c*** as A, G, C, or T to correspond to the third nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

n. selecting Im as the X_3 carboxamide residue and Py as the X_6 carboxamide residue if ***c*** = G;

o. selecting Py as the X_3 carboxamide residue and Im as the X_6 carboxamide residue if ***c*** = C;

p. selecting Hp as the X_3 carboxamide residue and Py as the X_6 carboxamide residue if ***c*** = T;

q. selecting Py as the X_3 carboxamide residue and Hp as the X_6 carboxamide residue if ***c*** = A;

r. defining ***d*** as A, G, C, or T to correspond to the fourth nucleotide to be bound by a carboxamide residue in the identified six base pair sequence;

s. selecting Im as the X_4 carboxamide residue and Py as the X_5 carboxamide residue if ***d*** = G;

t. selecting Py as the X_4 carboxamide residue and Im as the X_5 carboxamide residue if ***d*** = C;

u. selecting Hp as the X_4 carboxamide residue and Py as the X_5 carboxamide residue if ***d*** = T;

v. selecting Py as the X_4 carboxamide residue and Hp as the X_5 carboxamide residue if ***d*** = A; and

w. synthesizing the polyamide $X_1X_2X_3X_4$-γ-$X_5X_6X_7X_8$.

13. The polyamides described by the formulas listed in Tables 4 – 19.

14. The polyamides described by the formulas listed in Tables 20 – 83.

15. The polyamides described by the formulas listed in Tables 84 – 179.

16. A method for designing a selective polyamide molecule $X_1X_2X_3X_4X_5$-γ-$X_6X_7X_8X_9X_{10}$, wherein X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, and X_{10} are carboxamide residues forming binding pairs X_1/X_{10}, X_2/X_9, X_3/X_8, X_4/X_7, and X_5/X_6, and γ is γ-aminobuytic acid or 2,4 diaminobutyric acid suitable for binding to a six base pair sequence of the form 5'-WNNNNNW-3' in the minor groove of double stranded DNA, comprising the steps of:

a. identifying a seven base pair sequence of double stranded DNA having the form 5'-WNNNNNW-3', wherein W is either A or T, NNNNN is the sequence to be bound by carboxamide residues, and each N is independently A, G, C, or T;

b. representing the identified sequence as 5'-W***abcde***W-3', wherein ***a*** is a first nucleotide to be bound by a carboxamide residue, ***b*** is a second nucleotide to be

bound by a carboxamide residue, ***c*** is a third nucleotide to be bound by a carboxamide residue, ***d*** is a fourth nucleotide to be bound by a carboxamide residue, and ***e*** is a fifth nucleotide to be bound by a carboxamide residue;

c. defining ***a*** as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified seven base pair sequence;

d. selecting Im as the X_1 carboxamide residue and Py as the X_{10} carboxamide residue if ***a*** = G;

e. selecting Py as the X_1 carboxamide residue and Im as the X_{10} carboxamide residue if ***a*** = C;

f. selecting Hp as the X_1 carboxamide residue and Py as the X_{10} carboxamide residue if ***a*** = T;

g. selecting Py as the X_1 carboxamide residue and Hp as the X_{10} carboxamide residue if ***a*** = A;

h. defining ***b*** as A, G, C, or T to correspond to the second nucleotide to be bound by a carboxamide residue in the identified seven base pair sequence;

i. selecting Im as the X_2 carboxamide residue and Py as the X_9 carboxamide residue if ***b*** = G;

j. selecting Py as the X_2 carboxamide residue and Im as the X_9 carboxamide residue if ***b*** = C;

k. selecting Hp as the X_2 carboxamide residue and Py as the X_9 carboxamide residue if ***b*** = T;

l. selecting Py as the X_2 carboxamide residue and Hp as the X_9 carboxamide residue if ***b*** = A;

m. defining ***c*** as A, G, C, or T to correspond to the third nucleotide to be bound by a carboxamide residue in the identified seven base pair sequence;

n. selecting Im as the X_3 carboxamide residue and Py as the X_8 carboxamide residue if ***c*** = G;

o. selecting Py as the X_3 carboxamide residue and Im as the X_8 carboxamide residue if ***c*** = C;

p. selecting Hp as the X_3 carboxamide residue and Py as the X_8 carboxamide residue if ***c*** = T;

q. selecting Py as the X_3 carboxamide residue and Hp as the X_8 carboxamide residue if ***c*** = A;

r. defining ***d*** as A, G, C, or T to correspond to the fourth nucleotide to be bound by a carboxamide residue in the seven base pair sequence identified sequence;

s. selecting Im as the X_4 carboxamide residue and Py as the X_7 carboxamide residue if ***d*** = G;

t. selecting Py as the X_4 carboxamide residue and Im as the X_7 carboxamide residue if ***d*** = C;

u. selecting Hp as the X_4 carboxamide residue and Py as the X_7 carboxamide residue if ***d*** = T;

v. selecting Py as the X_4 carboxamide residue and Hp as the X_7 carboxamide residue if ***d*** = A;

w. defining ***e*** as A, G, C, or T to correspond to the fifth nucleotide to be bound by a carboxamide residue in the seven base pair sequence identified sequence;

x. selecting Im as the X_5 carboxamide residue and Py as the X_6 carboxamide residue if ***e*** = G;

y. selecting Py as the X_5 carboxamide residue and Im as the X_6 carboxamide residue if ***e*** = C;

z. selecting Hp as the X_5 carboxamide residue and Py as the X_6 carboxamide residue if ***e*** = T; and

aa. selecting Py as the X_5 carboxamide residue and Hp as the X_6 carboxamide residue if ***e*** = A.

17. The method of claim 16 further comprising the step of synthesizing the polyamide $X_1X_2X_3X_4X_5$-γ-$X_6X_7X_8X_9X_{10}$,.

18. The method of claim 17 further comprising the step of determining if the binding affinity of the polyamide to the identified sequence is subnanomolar.

19. The method of claim 17 further comprising the step of determining if the sequence specificity of the polyamide is greater or equal to ten.

20. The method of claim 17 further comprising the step of replacing at least one pyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_4, X_7, X_8, and X_9.

21. The method of claim 17 further comprising the step of replacing at least one 3-hydroxypyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_4, X_7, X_8, and X_9.

22. A polyamide composition produced by the method of claim 17.

23. A polyamide composition produced by the method of claim 18.

24. A polyamide composition produced by the method of claim 19.

25. A polyamide composition produced by the method of claim 20.

26. A polyamide composition produced by the method of claim 21.

27. A method for designing a selective polyamide molecule

$X_1X_2X_3X_4X_5X_6$-γ-$X_7X_8X_9X_{10}X_{11}X_{12}$,

wherein X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, X_{10} X_{11}, and X_{12}, are carboxamide residues forming binding pairs X_1/X_{12}, X_2/X_{11}, X_3/X_{10}, X_4/X_9, X_5/X_8, and X_6/X_7, and γ is γ-aminobuytic acid or 2,4 diaminobutyric acid

suitable for binding to a eight base pair sequence of the form 5'-WNNNNNNW-3' in the minor groove of double stranded DNA, comprising the steps of:

a. identifying a eight base pair sequence of double stranded DNA having the form 5'-WNNNNNNW-3', wherein W is either A or T, NNNNNN is the sequence to be bound by carboxamide residues, and each N is independently A, G, C, or T;

b. representing the identified sequence as 5'-W***abcdef***W-3', wherein ***a*** is a first nucleotide to be bound by a carboxamide residue, ***b*** is a second nucleotide to be bound by a carboxamide residue, ***c*** is a third nucleotide to be bound by a carboxamide residue, ***d*** is a fourth nucleotide to be bound by a carboxamide residue, ***e*** is a fifth nucleotide to be bound by a carboxamide residue and ***f*** is a sixth nucleotide to be bound by a carboxamide residue;

c. defining ***a*** as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified eight base pair sequence;

d. selecting Im as the X_1 carboxamide residue and Py as the X_{12} carboxamide residue if ***a*** = G;

e. selecting Py as the X_1 carboxamide residue and Im as the X_{10} carboxamide residue if ***a*** = C;

f. selecting Hp as the X_1 carboxamide residue and Py as the X_{12} carboxamide residue if ***a*** = T;

g. selecting Py as the X_1 carboxamide residue and Hp as the X_{12} carboxamide residue if ***a*** = A;

h. defining ***b*** as A, G, C, or T to correspond to the second nucleotide to be bound by a carboxamide residue in the identified eight base pair sequence;

i. selecting Im as the X_2 carboxamide residue and Py as the X_{11} carboxamide residue if ***b*** = G;

j. selecting Py as the X_2 carboxamide residue and Im as the X_{11} carboxamide residue if ***b*** = C;

k. selecting Hp as the X_2 carboxamide residue and Py as the X_{11} carboxamide residue if ***b*** = T;

l. selecting Py as the X_2 carboxamide residue and Hp as the X_{11} carboxamide residue if ***b*** = A;

m. defining ***c*** as A, G, C, or T to correspond to the third nucleotide to be bound by a carboxamide residue in the identified eight base pair sequence;

n. selecting Im as the X_3 carboxamide residue and Py as the X_{10} carboxamide residue if ***c*** = G;

o. selecting Py as the X_3 carboxamide residue and Im as the X_{10} carboxamide residue if ***c*** = C;

p. selecting Hp as the X_3 carboxamide residue and Py as the X_{10} carboxamide residue if ***c*** = T;

q. selecting Py as the X_3 carboxamide residue and Hp as the X_{10} carboxamide residue if ***c*** = A;

r. defining ***d*** as A, G, C, or T to correspond to the fourth nucleotide to be bound by a carboxamide residue in the eight base pair sequence identified sequence;

s. selecting Im as the X_4 carboxamide residue and Py as the X_9 carboxamide residue if ***d*** = G;

t. selecting Py as the X_4 carboxamide residue and Im as the X_9 carboxamide residue if ***d*** = C;

u. selecting Hp as the X_4 carboxamide residue and Py as the X_9 carboxamide residue if ***d*** = T;

v. selecting Py as the X_4 carboxamide residue and Hp as the X_9 carboxamide residue if ***d*** = A;

w. defining ***e*** as A, G, C, or T to correspond to the fifth nucleotide to be bound by a carboxamide residue in the eight base pair sequence identified sequence;

x. selecting Im as the X_5 carboxamide residue and Py as the X_8 carboxamide residue if ***e*** = G;

y. selecting Py as the X_5 carboxamide residue and Im as the X_8 carboxamide residue if e = C;

z. selecting Hp as the X_5 carboxamide residue and Py as the X_8 carboxamide residue if e = T;

aa. selecting Py as the X_5 carboxamide residue and Hp as the X_8 carboxamide residue if e = A;

bb. defining f as A, G, C, or T to correspond to the sixth nucleotide to be bound by a carboxamide residue in the eight base pair sequence identified sequence;

cc. selecting Im as the X_6 carboxamide residue and Py as the X_7 carboxamide residue if f = G;

dd. selecting Py as the X_6 carboxamide residue and Im as the X_7 carboxamide residue if f = C;

ee. selecting Hp as the X_6 carboxamide residue and Py as the X_7 carboxamide residue if f = T; and

ff. selecting Py as the X_6 carboxamide residue and Hp as the X_7 carboxamide residue if f = A.

28. The method of claim 17 further comprising the step of synthesizing the polyamide $X_1X_2X_3X_4X_5X_6$-γ-$X_7X_8X_9X_{10}X_{11}X_{12}$.

29. The method of claim 28 further comprising the step of determining if the binding affinity of the polyamide to the identified sequence is subnanomolar.

30. The method of claim 28 further comprising the step of determining if the sequence specificity of the polyamide is greater or equal to ten.

31. The method of claim 28 further comprising the step of replacing at least one pyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_4, X_5, X_8, X_9, X_{10}, and X_{11}.

32. The method of claim 28 further comprising the step of replacing at least one 3-hydroxypyrrole residue with a β-alanine residue at a position chosen from the group consisting of X_2, X_3, X_4, X_5, X_8, X_9, X_{10}, and X_{11}.

33. A polyamide composition produced by the method of claim 28.

34. A polyamide composition produced by the method of claim 29.

35. A polyamide composition produced by the method of claim 30.

36. A polyamide composition produced by the method of claim 31.

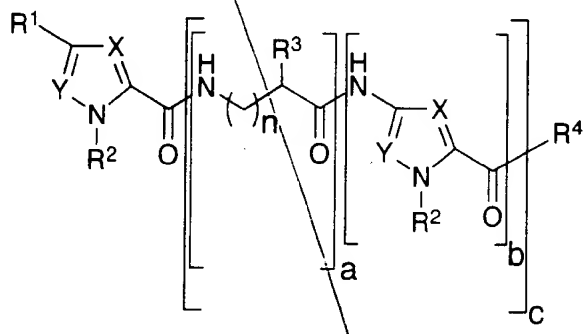
37. A polyamide composition produced by the method of claim 32.

38. A polyamide composition produced by the method of claim 2 wherein one carboxamide binding pair is β/β.

39. A polyamide composition produced by the method of claim 7 wherein one carboxamide binding pair is β/β.

40. A polyamide composition produced by the method of claim 17 wherein one carboxamide binding pair is β/β.

41. A selective polyamide according to claim 1 whereby the polyamide is of the formula:



or a pharmaceutically acceptable salt wherein:

R^1 is chosen from H, NH_2, SH, Cl, Br, F, N-acetyl, or N-formyl;

R^2 is chosen from H, $(CH_2)_mCH_3$, $(CH_2)_mNH_2$, $(CH_2)_mSH$, $(CH_2)_mOH$, $(CH_2)_mNR^5{}_2$, $(CH_2)_mOR^5$, $(CH_2)_mSR^5$, where R^5 = $(CH_2)_mCH_3$, $(CH_2)_mNH_2$, $(CH_2)_mSH$, $(CH_2)_mOH$ and m is an integer from 0 to 6;

R^3 is chosen from H, NH_2, OH, SH, Br, Cl, F, OMe, CH_2OH, CH_2SH, CH_2NH_2;

R^4 is chosen from $-NH(CH_2)_{0\text{-}100}NR^6R^7$ or $NH(CH_2)_pCO\ NH(CH_2)_{0\text{-}100}NR^6R^7$ or NHR^6 or $NH(CH_2)_pCONHR^6$, where R^6 and R^7 are independently chosen from H, Cl, NO, N-acetyl, benzyl, $C_{1\text{-}100}$ alkyl, $C_{1\text{-}100}$ alkylamine, $C_{1\text{-}100}$ alkyldiamine, $C_{1\text{-}100}$ alkylcarboxylate, $C_{1\text{-}100}$ alkenyl, a $C_{1\text{-}100}$ alkynyl, or a $C_{1\text{-}100}L$, where L groups can be independently chosen from but is not limited to arylboronic acids, biotins, polyhistidines comprised from about 2 to 8 amino acids, haptens to which an antibody binds, solid phase supports, oligodeoxynucleotide, N-ethylnitrosourea, fluorescein, bromoacetamide, iodoacetamide, DL-α-lipoic acid, acridine, captothesin, pyrene, mitomycin, texas red, anthracene, anthrinilic acid, avidin, DAPI, an oligodeoxynucleotide, isosulfan blue, malachite green, psoralen, ethyl red, 4-(psoraen-8-yloxy)-butyrate, tartaric acid, (+)-α-tocopheral;

where X and Y are chosen from the group consisting of N, CH, COH, CCH_3, CNH_2, CCl, CF;

a is an integer having values of 0 or 1;

b is an integer ranging from 1 to 5 inclusive; and

c is an integer value ranging from 2 to 10 inclusive.

42. The polyamide of claim 1 wherein the duplex DNA sequence is a regulatory sequence.

43. The polyamide of claim 1 wherein the duplex DNA sequence is a promoter sequence.

44. The polyamide of claim 1 wherein the duplex DNA sequence is a coding sequence.

45. The polyamide of claim 1 wherein the duplex DNA sequence is a non-coding sequence.

46. The polyamide of claim 1 wherein the binding of the carboxamide binding pairs to the identified target DNA sequence modulates the expression of a gene.

47. A composition conprising an effective amount of the polyamide of claim 1 and a pharmologically suitable excipient.

48. A diagnostic kit comprising the polyamide of claim 1.